

SEQUENCE LISTING

<110> CHOO, Qui-Lim
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<120> METHODS AND REAGENTS FOR TREATING, PREVENTING AND DIAGNOSING
BUNYAVIRUS INFECTION

<130> 21454

<140> US 10/580,050

<141> 2006-05-19

<150> PCT/US04/039333

<151> 2004-11-19

<160> 191

<170> PatentIn version 3.3

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<212> DNA

<213> La Crosse virus

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Ala Lys Ala Ala Leu Ser Arg Lys Pro Glu Arg Lys Ala Asn Pro Lys
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Phe Gly Glu Trp Gln Val Glu Val Ile Asn Asn His Phe Pro Gly Asn
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Gly Tyr Leu Ala Arg Trp Val Leu Asp Gln Tyr Asn Glu Asn Asp Asp

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acagaaccca	gcacaattat	ttatagaaca	gatattgttc	tcacataagc	ccataataga	4620

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agaatttgat tagtagttat gagtttacag agaacctaca attaggctat aaatttgga 6900
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gtagataggg gcacactact

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<210> 6
<211> 2263
<212> PRT
<213> La Crosse virus

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Arg Asp Ala Cys Val Ala Lys Asp Ile Asp Val Asp Leu Leu Met Ala
20 25 30

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Arg His Asp Tyr Phe Gly Arg Glu Leu Cys Lys Ser Leu Asn Ile Glu

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35	40	45
Tyr Arg Asn Asp Val Pro Phe Val Asp Ile Ile Leu Asp Ile Arg Pro		
50	55	60
Glu Val Asp Pro Leu Thr Ile Asp Ala Pro His Ile Thr Pro Asp Asn		
65	70	75 80
Tyr Leu Tyr Ile Asn Asn Val Leu Tyr Ile Ile Asp Tyr Lys Val Ser		
	85	90 95
Val Ser Asn Glu Ser Ser Val Ile Thr Tyr Asp Lys Tyr Tyr Glu Leu		
	100	105 110
Thr Arg Asp Ile Ser Asp Arg Leu Ser Ile Pro Ile Glu Ile Val Ile		
	115	120 125
Val Arg Ile Asp Pro Val Ser Lys Asp Leu His Ile Asn Ser Asp Arg		
	130	135 140
Phe Lys Glu Leu Tyr Pro Thr Ile Val Val Asp Ile Asn Phe Asn Gln		
145	150	155 160
Phe Phe Asp Leu Lys Gln Leu Leu Tyr Glu Lys Phe Gly Asp Asp Glu		
	165	170 175
Glu Phe Leu Leu Lys Val Ala His Gly Asp Phe Thr Leu Thr Ala Pro		
	180	185 190
Trp Cys Lys Thr Gly Cys Pro Glu Phe Trp Lys His Pro Ile Tyr Lys		
	195	200 205
Glu Phe Lys Met Ser Met Pro Val Pro Glu Arg Arg Leu Phe Glu Glu		
	210	215 220
Ser Val Lys Phe Asn Ala Tyr Glu Ser Glu Arg Trp Asn Thr Asn Leu		
225	230	235 240
Val Lys Ile Arg Glu Tyr Thr Lys Lys Asp Tyr Ser Glu His Ile Ser		
	245	250 255
Lys Ser Ala Lys Asn Ile Phe Leu Ala Ser Gly Phe Tyr Lys Gln Pro		
	260	265 270
Asn Lys Asn Glu Ile Ser Glu Gly Trp Thr Leu Met Val Glu Arg Val		
	275	280 285
Gln Asp Gln Arg Glu Ile Ser Lys Ser Leu His Asp Gln Lys Pro Ser		
	290	295 300
Ile His Phe Ile Trp Gly Ala His Asn Pro Gly Asn Ser Asn Asn Ala		
305	310	315 320
Thr Phe Lys Leu Ile Leu Leu Ser Lys Ser Leu Gln Ser Ile Lys Gly		
	325	330 335

Ile	Ser	Thr	Tyr	Thr	Glu	Ala	Phe	Lys	Ser	Leu	Gly	Lys	Met	Met	Asp	340	345	350	
Ile	Gly	Asp	Lys	Ala	Ile	Glu	Tyr	Glu	Glu	Phe	Cys	Met	Ser	Leu	Lys	355	360	365	
Ser	Lys	Ala	Arg	Ser	Ser	Trp	Lys	Gln	Ile	Met	Asn	Lys	Lys	Leu	Glu	370	375	380	
Pro	Lys	Gln	Ile	Asn	Asn	Ala	Leu	Val	Leu	Trp	Glu	Gln	Gln	Phe	Met	385	390	395	400
Val	Asn	Asn	Asp	Leu	Ile	Asp	Lys	Ser	Glu	Lys	Leu	Lys	Leu	Phe	Lys	405	410	415	
Asn	Phe	Cys	Gly	Ile	Gly	Lys	His	Lys	Gln	Phe	Lys	Asn	Lys	Met	Leu	420	425	430	
Glu	Asp	Leu	Glu	Val	Ser	Lys	Pro	Lys	Ile	Leu	Asp	Phe	Asp	Asp	Ala	435	440	445	
Asn	Met	Tyr	Leu	Ala	Ser	Leu	Thr	Met	Met	Glu	Gln	Ser	Lys	Lys	Ile	450	455	460	
Leu	Ser	Lys	Ser	Asn	Gly	Leu	Lys	Pro	Asp	Asn	Phe	Ile	Leu	Asn	Glu	465	470	475	480
Phe	Gly	Ser	Lys	Ile	Lys	Asp	Ala	Asn	Lys	Glu	Thr	Tyr	Asp	Asn	Met	485	490	495	
His	Lys	Ile	Phe	Glu	Thr	Arg	Tyr	Trp	Gln	Cys	Ile	Ser	Asp	Phe	Ser	500	505	510	
Thr	Leu	Met	Lys	Asn	Ile	Leu	Ser	Val	Ser	Gln	Tyr	Asn	Arg	His	Asn	515	520	525	
Thr	Phe	Arg	Ile	Ala	Met	Cys	Ala	Asn	Asn	Asn	Val	Phe	Ala	Ile	Val	530	535	540	
Phe	Pro	Ser	Ala	Asp	Ile	Lys	Thr	Lys	Lys	Ala	Thr	Val	Val	Tyr	Ser	545	550	555	560
Ile	Ile	Val	Leu	His	Lys	Glu	Glu	Glu	Asn	Ile	Phe	Asn	Pro	Gly	Cys	565	570	575	
Leu	His	Gly	Thr	Phe	Lys	Cys	Met	Asn	Gly	Tyr	Ile	Ser	Ile	Ser	Arg	580	585	590	
Ala	Ile	Arg	Leu	Asp	Lys	Glu	Arg	Cys	Gln	Arg	Ile	Val	Ser	Ser	Pro	595	600	605	
Gly	Leu	Phe	Leu	Thr	Thr	Cys	Leu	Leu	Phe	Lys	His	Asp	Asn	Pro	Thr	610	615	620	

Leu Val Met Ser Asp Ile Met Asn Phe Ser Ile Tyr Thr Ser Leu Ser
 625 630 635 640
 Ile Thr Lys Ser Val Leu Ser Leu Thr Glu Pro Ala Arg Tyr Met Ile
 645 650 655
 Met Asn Ser Leu Ala Ile Ser Ser Asn Val Lys Asp Tyr Ile Ala Glu
 660 665 670
 Lys Phe Ser Pro Tyr Thr Lys Thr Leu Phe Ser Val Tyr Met Thr Arg
 675 680 685
 Leu Ile Lys Asn Ala Cys Phe Asp Ala Tyr Asp Gln Arg Gln Arg Val
 690 695 700
 Gln Leu Arg Asp Ile Tyr Leu Ser Asp Tyr Asp Ile Thr Gln Lys Gly
 705 710 715 720
 Ile Lys Asp Asn Arg Glu Leu Thr Ser Ile Trp Phe Pro Gly Ser Val
 725 730 735
 Thr Leu Lys Glu Tyr Leu Thr Gln Ile Tyr Leu Pro Phe Tyr Phe Asn
 740 745 750
 Ala Lys Gly Leu His Glu Lys His His Val Met Val Asp Leu Ala Lys
 755 760 765
 Thr Ile Leu Glu Ile Glu Cys Glu Gln Arg Glu Asn Ile Lys Glu Ile
 770 775 780
 Trp Ser Thr Asn Cys Thr Lys Gln Thr Val Asn Leu Lys Ile Leu Ile
 785 790 795 800
 His Ser Leu Cys Lys Asn Leu Leu Ala Asp Thr Ser Arg His Asn His
 805 810 815
 Leu Arg Asn Arg Ile Glu Asn Arg Asn Asn Phe Arg Arg Ser Ile Thr
 820 825 830
 Thr Ile Ser Thr, Phe Thr Ser Ser Lys Ser Cys Leu Lys Ile Gly Asp
 835 840 845
 Phe Arg Lys Glu Lys Glu Leu Gln Ser Val Lys Gln Lys Lys Ile Leu
 850 855 860
 Glu Val Gln Ser Arg Lys Met Arg Leu Ala Asn Pro Met Phe Val Thr
 865 870 875 880
 Asp Glu Gln Val Cys Leu Glu Val Gly His Cys Asn Tyr Glu Met Leu
 885 890 895
 Arg Asn Ala Met Pro Asn Tyr Thr Asp Tyr Ile Ser Thr Lys Val Phe
 900 905 910
 Asp Arg Leu Tyr Glu Leu Leu Asp Lys Gly Val Leu Thr Asp Lys Pro

915	920	925
Val Ile Glu Gln Ile Met Asp Met Met Val Asp His Lys Lys Phe Tyr		
930	935	940
Phe Thr Phe Phe Asn Lys Gly Gln Lys Thr Ser Lys Asp Arg Glu Ile		
945	950	955 960
Phe Val Gly Glu Tyr Glu Ala Lys Met Cys Met Tyr Ala Val Glu Arg		
	965	970 975
Ile Ala Lys Glu Arg Cys Lys Leu Asn Pro Asp Glu Met Ile Ser Glu		
	980	985 990
Pro Gly Asp Gly Lys Leu Lys Val Leu Glu Gln Lys Ser Glu Gln Glu		
	995	1000 1005
Ile Arg Phe Leu Val Glu Thr Thr Arg Gln Lys Asn Arg Glu Ile		
1010	1015	1020
Asp Glu Ala Ile Glu Ala Leu Ala Ala Glu Gly Tyr Glu Ser Asn		
1025	1030	1035
Leu Glu Lys Ile Glu Lys Leu Ser Leu Gly Lys Ala Lys Gly Leu		
1040	1045	1050
Lys Met Glu Ile Asn Ala Asp Met Ser Lys Trp Ser Ala Gln Asp		
1055	1060	1065
Val Phe Tyr Lys Tyr Phe Trp Leu Ile Ala Leu Asp Pro Ile Leu		
1070	1075	1080
Tyr Pro Gln Glu Lys Glu Arg Ile Leu Tyr Phe Met Cys Asn Tyr		
1085	1090	1095
Met Asp Lys Glu Leu Ile Leu Pro Asp Glu Leu Leu Phe Asn Leu		
1100	1105	1110
Leu Asp Gln Lys Val Ala Tyr Gln Asn Asp Ile Ile Ala Thr Met		
1115	1120	1125
Thr Asn Gln Leu Asn Ser Asn Thr Val Leu Ile Lys Arg Asn Trp		
1130	1135	1140
Leu Gln Gly Asn Phe Asn Tyr Thr Ser Ser Tyr Val His Ser Cys		
1145	1150	1155
Ala Met Ser Val Tyr Lys Glu Ile Leu Lys Glu Ala Ile Thr Leu		
1160	1165	1170
Leu Asp Gly Ser Ile Leu Val Asn Ser Leu Val His Ser Asp Asp		
1175	1180	1185
Asn Gln Thr Ser Ile Thr Ile Val Gln Asp Lys Met Glu Asn Asp		
1190	1195	1200

Lys	Ile	Ile	Asp	Phe	Ala	Met	Lys	Glu	Phe	Glu	Arg	Ala	Cys	Leu
1205						1210					1215			
Thr	Phe	Gly	Cys	Gln	Ala	Asn	Met	Lys	Lys	Thr	Tyr	Val	Thr	Asn
1220						1225					1230			
Cys	Ile	Lys	Glu	Phe	Val	Ser	Leu	Phe	Asn	Leu	Tyr	Gly	Glu	Pro
1235						1240					1245			
Phe	Ser	Ile	Tyr	Gly	Arg	Phe	Leu	Leu	Thr	Ser	Val	Gly	Asp	Cys
1250						1255					1260			
Ala	Tyr	Ile	Gly	Pro	Tyr	Glu	Asp	Leu	Ala	Ser	Arg	Ile	Ser	Ser
1265						1270					1275			
Ala	Gln	Thr	Ala	Ile	Lys	His	Gly	Cys	Pro	Pro	Ser	Leu	Ala	Trp
1280						1285					1290			
Val	Ser	Ile	Ala	Ile	Ser	His	Trp	Met	Thr	Ser	Leu	Thr	Tyr	Asn
1295						1300					1305			
Met	Leu	Pro	Gly	Gln	Ser	Asn	Asp	Pro	Ile	Asp	Tyr	Phe	Pro	Ala
1310						1315					1320			
Glu	Asn	Arg	Lys	Asp	Ile	Pro	Ile	Glu	Leu	Asn	Gly	Val	Leu	Asp
1325						1330					1335			
Ala	Pro	Leu	Ser	Met	Ile	Ser	Thr	Val	Gly	Leu	Glu	Ser	Gly	Asn
1340						1345					1350			
Leu	Tyr	Phe	Leu	Ile	Lys	Leu	Leu	Ser	Lys	Tyr	Thr	Pro	Val	Met
1355						1360					1365			
Gln	Lys	Arg	Glu	Ser	Val	Val	Asn	Gln	Ile	Ala	Glu	Val	Lys	Asn
1370						1375					1380			
Trp	Lys	Val	Glu	Asp	Leu	Thr	Asp	Asn	Glu	Ile	Phe	Arg	Leu	Lys
1385						1390					1395			
Ile	Leu	Arg	Tyr	Leu	Val	Leu	Asp	Ala	Glu	Met	Asp	Pro	Ser	Asp
1400						1405					1410			
Ile	Met	Gly	Glu	Thr	Ser	Asp	Met	Arg	Gly	Arg	Ser	Ile	Leu	Thr
1415						1420					1425			
Pro	Arg	Lys	Phe	Thr	Thr	Ala	Gly	Ser	Leu	Arg	Lys	Leu	Tyr	Ser
1430						1435					1440			
Phe	Ser	Lys	Tyr	Gln	Asp	Arg	Leu	Ser	Ser	Pro	Gly	Gly	Met	Val
1445						1450					1455			
Glu	Leu	Phe	Thr	Tyr	Leu	Leu	Glu	Lys	Pro	Glu	Leu	Leu	Val	Thr
1460						1465					1470			

Lys Gly	Glu Asp Met Lys Asp	Tyr Met Glu Ser Val	Ile Phe Arg
1475	1480	1485	
Tyr Asn	Ser Lys Arg Phe Lys	Glu Ser Leu Ser Ile	Gln Asn Pro
1490	1495	1500	
Ala Gln	Leu Phe Ile Glu Gln	Ile Leu Phe Ser His	Lys Pro Ile
1505	1510	1515	
Ile Asp	Phe Ser Gly Ile Arg	Asp Lys Tyr Ile Asn	Leu His Asp
1520	1525	1530	
Ser Arg	Ala Leu Glu Lys Glu	Pro Asp Ile Leu Gly	Lys Val Thr
1535	1540	1545	
Phe Thr	Glu Ala Tyr Arg Leu	Leu Met Arg Asp Leu	Ser Ser Leu
1550	1555	1560	
Glu Leu	Thr Asn Asp Asp Ile	Gln Val Ile Tyr Ser	Tyr Ile Ile
1565	1570	1575	
Leu Asn	Asp Pro Met Met Ile	Thr Ile Ala Asn Thr	His Ile Leu
1580	1585	1590	
Ser Ile	Tyr Gly Ser Pro Gln	Arg Arg Met Gly Met	Ser Cys Ser
1595	1600	1605	
Thr Met	Pro Glu Phe Arg Asn	Leu Lys Leu Ile His	His Ser Pro
1610	1615	1620	
Ala Leu	Val Leu Arg Ala Tyr	Ser Lys Asn Asn Pro	Asp Ile Gln
1625	1630	1635	
Gly Ala	Asp Pro Thr Glu Met	Ala Arg Asp Leu Val	His Leu Lys
1640	1645	1650	
Glu Phe	Val Glu Asn Thr Asn	Leu Glu Glu Lys Met	Lys Val Arg
1655	1660	1665	
Ile Ala	Ile Asn Glu Ala Glu	Lys Gly Gln Arg Asp	Ile Val Phe
1670	1675	1680	
Glu Leu	Lys Glu Met Thr Arg	Phe Tyr Gln Val Cys	Tyr Glu Tyr
1685	1690	1695	
Val Lys	Ser Thr Glu His Lys	Ile Lys Val Phe Ile	Leu Pro Thr
1700	1705	1710	
Lys Ser	Tyr Thr Thr Thr Asp	Phe Cys Ser Leu Met	Gln Gly Asn
1715	1720	1725	
Leu Ile	Lys Asp Lys Glu Trp	Tyr Thr Val His Tyr	Leu Lys Gln
1730	1735	1740	
Ile Leu	Ser Gly Gly His Lys	Ala Ile Met Gln His	Asn Ala Thr

1745	1750	1755
Ser Glu Gln Asn Ile Ala Phe	Glu Cys Phe Lys Leu	Ile Thr His
1760	1765	1770
Phe Ala Asp Ser Phe Ile Asp	Ser Leu Ser Arg Ser	Ala Phe Leu
1775	1780	1785
Gln Leu Ile Ile Asp Glu Phe	Ser Tyr Lys Asp Val	Lys Val Ser
1790	1795	1800
Lys Leu Tyr Asp Ile Ile Lys	Asn Gly Tyr Asn Arg	Thr Asp Phe
1805	1810	1815
Ile Pro Leu Leu Phe Arg Thr	Gly Asp Leu Arg Gln	Ala Asp Leu
1820	1825	1830
Asp Lys Tyr Asp Ala Met Lys	Ser His Glu Arg Val	Thr Trp Asn
1835	1840	1845
Asp Trp Gln Thr Ser Arg His	Leu Asp Met Gly Ser	Ile Asn Leu
1850	1855	1860
Thr Ile Thr Gly Tyr Asn Arg	Ser Ile Thr Ile Ile	Gly Glu Asp
1865	1870	1875
Asn Lys Leu Thr Tyr Ala Glu	Leu Cys Leu Thr Arg	Lys Thr Pro
1880	1885	1890
Glu Asn Ile Thr Ile Ser Gly	Arg Lys Leu Leu Gly	Ala Arg His
1895	1900	1905
Gly Leu Lys Phe Glu Asn Met	Ser Lys Ile Gln Thr	Tyr Pro Gly
1910	1915	1920
Asn Tyr Tyr Ile Thr Tyr Arg	Lys Lys Asp Arg His	Gln Phe Val
1925	1930	1935
Tyr Gln Ile His Ser His Glu	Ser Ile Thr Arg Arg	Asn Glu Glu
1940	1945	1950
His Met Ala Ile Arg Thr Arg	Ile Tyr Asn Glu Ile	Thr Pro Val
1955	1960	1965
Cys Val Val Asn Val Ala Glu	Val Asp Gly Asp Gln	Arg Ile Leu
1970	1975	1980
Ile Arg Ser Leu Asp Tyr Leu	Asn Asn Asp Ile Phe	Ser Leu Ser
1985	1990	1995
Arg Ile Lys Val Gly Leu Asp	Glu Phe Ala Thr Ile	Lys Lys Ala
2000	2005	2010
His Phe Ser Lys Met Val Ser	Phe Glu Gly Pro Pro	Ile Lys Thr
2015	2020	2025

Gly	Leu	Leu	Asp	Leu	Thr	Glu	Leu	Met	Lys	Ser	Gln	Asp	Leu	Leu
2030						2035					2040			
Asn	Leu	Asn	Tyr	Asp	Asn	Ile	Arg	Asn	Ser	Asn	Leu	Ile	Ser	Phe
2045						2050					2055			
Ser	Lys	Leu	Ile	Cys	Cys	Glu	Gly	Ser	Asp	Asn	Ile	Asn	Asp	Gly
2060						2065					2070			
Leu	Glu	Phe	Leu	Ser	Asp	Asp	Pro	Met	Asn	Phe	Thr	Glu	Gly	Glu
2075						2080					2085			
Ala	Ile	His	Ser	Thr	Pro	Ile	Phe	Asn	Ile	Tyr	Tyr	Ser	Lys	Arg
2090						2095					2100			
Gly	Glu	Arg	His	Met	Thr	Tyr	Arg	Asn	Ala	Ile	Lys	Leu	Leu	Ile
2105						2110					2115			
Glu	Arg	Glu	Thr	Lys	Ile	Phe	Glu	Glu	Ala	Phe	Thr	Phe	Ser	Glu
2120						2125					2130			
Asn	Gly	Phe	Ile	Ser	Pro	Glu	Asn	Leu	Gly	Cys	Leu	Glu	Ala	Val
2135						2140					2145			
Val	Ser	Leu	Ile	Lys	Leu	Leu	Lys	Thr	Asn	Glu	Trp	Ser	Thr	Val
2150						2155					2160			
Ile	Asp	Lys	Cys	Ile	His	Ile	Cys	Leu	Ile	Lys	Asn	Gly	Met	Asp
2165						2170					2175			
His	Met	Tyr	His	Ser	Phe	Asp	Val	Pro	Lys	Cys	Phe	Met	Gly	Asn
2180						2185					2190			
Pro	Ile	Thr	Arg	Asp	Met	Asn	Trp	Met	Met	Phe	Arg	Glu	Phe	Ile
2195						2200					2205			
Asn	Ser	Leu	Pro	Gly	Thr	Asp	Ile	Pro	Pro	Trp	Asn	Val	Met	Thr
2210						2215					2220			
Glu	Asn	Phe	Lys	Lys	Lys	Cys	Ile	Ala	Leu	Ile	Asn	Ser	Lys	Leu
2225						2230					2235			
Glu	Thr	Gln	Arg	Asp	Phe	Ser	Glu	Phe	Thr	Lys	Leu	Met	Lys	Lys
2240						2245					2250			
Glu	Gly	Gly	Arg	Ser	Asn	Ile	Glu	Phe	Asp					
2255						2260								

<210> 7
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Antisense primer derived from M segment of LACV genome

<400> 7
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<210> 8
 <211> 22
 <212> DNA
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<220>
 <223> Sense primer derived from M segment of LACV genome

<400> 8
 tggaaatggc atcgagaata aa 22

<210> 9
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Probe derived from M segment of LACV genome

<400> 9
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<210> 10
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sense primer derived from S segment of LACV genome

<400> 10
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<210> 11
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<220>
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<400> 11
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<210> 12
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<220>
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<400> 12
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<210> 13
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sense primer derived from L segment of LACV genome

<400> 13
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<210> 14
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Antisense primer derived from L segment of LACV genome

<400> 14
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<210> 15
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Probe derived from L segment of LACV genome

<400> 15
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<210> 16
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide specific for LACV sequence

<400> 16
catgagcat tcaaattagg ttcta

25

<210> 17
<211> 174
<212> PRT
<213> La Crosse virus

<400> 17
Val Met Cys Lys Ser Lys Gly Pro Ala Ser Ile Leu Ser Ile Ile Thr
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Ala Val Leu Val Leu Thr Phe Val Thr Pro Ile Asn Ser Met Val Leu
20 25 30
Gly Glu Ser Lys Glu Thr Phe Glu Leu Glu Asp Leu Pro Asp Asp Met
35 40 45
Leu Glu Met Ala Ser Arg Ile Asn Ser Tyr Tyr Leu Thr Cys Ile Leu
50 55 60
Asn Tyr Ala Val Ser Trp Gly Leu Val Ile Ile Gly Leu Leu Ile Gly
65 70 75 80
Leu Leu Phe Lys Lys Tyr Gln His Arg Phe Leu Asn Val Tyr Ala Met
85 90 95
Tyr Cys Glu Glu Cys Asp Met Tyr His Asp Lys Ser Gly Leu Lys Arg
100 105 110
His Gly Asp Phe Thr Asn Lys Cys Arg Gln Cys Thr Cys Gly Gln Tyr
115 120 125
Glu Asp Ala Ala Gly Leu Met Ala His Arg Lys Thr Tyr Asn Cys Leu
130 135 140
Val Gln Tyr Lys Ala Lys Trp Met Met Asn Phe Leu Ile Ile Tyr Ile
145 150 155 160
Phe Leu Ile Leu Ile Lys Asp Ser Ala Ile Val Val Gln Ala
165 170

<210> 18
<211> 968
<212> PRT
<213> La Crosse virus

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Lys	Lys	Glu	Pro	Tyr	Thr	Asn	Ile	Ala	Thr	Gln	Leu	Lys	Gly	Leu	Lys
		35					40					45			
Ala	Ile	Ser	Val	Leu	Asp	Val	Pro	Ile	Ile	Thr	Gly	Ile	Pro	Asp	Asp
		50					55					60			
Ile	Ala	Gly	Ala	Leu	Arg	Tyr	Ile	Glu	Glu	Lys	Glu	Asp	Phe	His	Val
							70					75			80
Gln	Leu	Thr	Ile	Glu	Tyr	Ala	Met	Leu	Ser	Lys	Tyr	Cys	Asp	Tyr	Tyr
															95
Thr	Gln	Phe	Ser	Asp	Asn	Ser	Gly	Tyr	Ser	Gln	Thr	Thr	Trp	Arg	Val
															110
Tyr	Leu	Arg	Ser	His	Asp	Phe	Glu	Ala	Cys	Ile	Leu	Tyr	Pro	Asn	Gln
															125
His	Phe	Cys	Arg	Cys	Val	Lys	Asn	Gly	Glu	Lys	Cys	Ser	Ser	Ser	Asn
															140
Trp	Asp	Phe	Ala	Asn	Glu	Met	Lys	Asp	Tyr	Tyr	Ser	Gly	Lys	Gln	Thr
															160
Lys	Phe	Asp	Lys	Asp	Leu	Asn	Leu	Ala	Leu	Thr	Ala	Leu	His	His	Ala
															175
Phe	Arg	Gly	Thr	Ser	Ser	Ala	Tyr	Ile	Ala	Thr	Met	Leu	Ser	Lys	Lys
															190
Ser	Asn	Asp	Asp	Leu	Ile	Ala	Tyr	Thr	Asn	Lys	Ile	Lys	Thr	Lys	Phe
															205
Pro	Gly	Asn	Ala	Leu	Leu	Lys	Ala	Ile	Ile	Asp	Tyr	Ile	Ala	Tyr	Met
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Lys	Ser	Leu	Pro	Gly	Met	Ala	Asn	Phe	Lys	Tyr	Asp	Glu	Phe	Trp	Asp
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Glu	Leu	Leu	Tyr	Lys	Pro	Asn	Pro	Ala	Lys	Ala	Ser	Asn	Leu	Ala	Arg
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Gly	Lys	Glu	Ser	Ser	Tyr	Asn	Phe	Lys	Leu	Ala	Ile	Ser	Ser	Lys	Ser
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Ile	Lys	Thr	Cys	Lys	Asn	Val	Lys	Asp	Val	Ala	Cys	Leu	Ser	Pro	Arg
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Ser	Gly	Ala	Ile	Tyr	Ala	Ser	Ile	Ile	Ala	Cys	Gly	Glu	Pro	Asn	Gly
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Pro	Ser	Val	Tyr	Arg	Lys	Pro	Ser	Gly	Gly	Val	Phe	Gln	Ser	Ser	Thr
															320

Asp	Arg	Ser	Ile	Tyr	Cys	Leu	Leu	Asp	Ser	His	Cys	Leu	Glu	Glu	Phe	325	330	335	
Glu	Ala	Ile	Gly	Gln	Glu	Glu	Leu	Asp	Ala	Val	Lys	Lys	Ser	Lys	Cys	340	345	350	
Trp	Glu	Ile	Glu	Tyr	Pro	Asp	Val	Lys	Leu	Ile	Gln	Glu	Gly	Asp	Gly	355	360	365	
Thr	Lys	Ser	Cys	Arg	Met	Lys	Asp	Ser	Gly	Asn	Cys	Asn	Val	Ala	Thr	370	375	380	
Asn	Arg	Trp	Pro	Val	Ile	Gln	Cys	Glu	Asn	Asp	Lys	Phe	Tyr	Tyr	Ser	385	390	395	400
Glu	Leu	Gln	Lys	Asp	Tyr	Asp	Lys	Ala	Gln	Asp	Ile	Gly	His	Tyr	Cys	405	410	415	
Leu	Ser	Pro	Gly	Cys	Thr	Thr	Val	Arg	Tyr	Pro	Ile	Asn	Pro	Lys	His	420	425	430	
Ile	Ser	Asn	Cys	Asn	Trp	Gln	Val	Ser	Arg	Ser	Ser	Ile	Ala	Lys	Ile	435	440	445	
Asp	Val	His	Asn	Ile	Glu	Asp	Ile	Glu	Gln	Tyr	Lys	Lys	Ala	Ile	Thr	450	455	460	
Gln	Lys	Leu	Gln	Thr	Ser	Leu	Ser	Leu	Phe	Lys	Tyr	Ala	Lys	Thr	Lys	465	470	475	480
Asn	Leu	Pro	His	Ile	Lys	Pro	Ile	Tyr	Lys	Tyr	Ile	Thr	Ile	Glu	Gly	485	490	495	
Thr	Glu	Thr	Ala	Glu	Gly	Ile	Glu	Ser	Ala	Tyr	Ile	Glu	Ser	Glu	Val	500	505	510	
Pro	Ala	Leu	Ala	Gly	Thr	Ser	Ile	Gly	Phe	Lys	Ile	Asn	Ser	Lys	Glu	515	520	525	
Gly	Lys	His	Leu	Leu	Asp	Val	Ile	Ala	Tyr	Val	Lys	Ser	Ala	Ser	Tyr	530	535	540	
Ser	Ser	Val	Tyr	Thr	Lys	Leu	Tyr	Ser	Thr	Gly	Pro	Thr	Ser	Gly	Ile	545	550	555	560
Asn	Thr	Lys	His	Asp	Glu	Leu	Cys	Thr	Gly	Pro	Cys	Pro	Ala	Asn	Ile	565	570	575	
Asn	His	Gln	Val	Gly	Trp	Leu	Thr	Phe	Ala	Arg	Glu	Arg	Thr	Ser	Ser	580	585	590	
Trp	Gly	Cys	Glu	Glu	Phe	Gly	Cys	Leu	Ala	Val	Ser	Asp	Gly	Cys	Val	595	600	605	

Phe	Gly	Ser	Cys	Gln	Asp	Ile	Ile	Lys	Glu	Glu	Leu	Ser	Val	Tyr	Arg	610	615	620	
Lys	Glu	Thr	Glu	Glu	Val	Thr	Asp	Val	Glu	Leu	Cys	Leu	Thr	Phe	Ser	625	630	635	640
Asp	Lys	Thr	Tyr	Cys	Thr	Asn	Leu	Asn	Pro	Val	Thr	Pro	Ile	Ile	Thr	645	650	655	
Asp	Leu	Phe	Glu	Val	Gln	Phe	Lys	Thr	Val	Glu	Thr	Tyr	Ser	Leu	Pro	660	665	670	
Arg	Ile	Val	Ala	Val	Gln	Asn	His	Glu	Ile	Lys	Ile	Gly	Gln	Ile	Asn	675	680	685	
Asp	Leu	Gly	Val	Tyr	Ser	Lys	Gly	Cys	Gly	Asn	Val	Gln	Lys	Val	Asn	690	695	700	
Gly	Thr	Ile	Tyr	Gly	Asn	Gly	Val	Pro	Arg	Phe	Asp	Tyr	Leu	Cys	His	705	710	715	720
Leu	Ala	Ser	Arg	Lys	Glu	Val	Ile	Val	Arg	Lys	Cys	Phe	Asp	Asn	Asp	725	730	735	
Tyr	Gln	Ala	Cys	Lys	Phe	Leu	Gln	Ser	Pro	Ala	Ser	Tyr	Arg	Leu	Glu	740	745	750	
Glu	Asp	Ser	Gly	Thr	Val	Thr	Ile	Ile	Asp	Tyr	Lys	Lys	Ile	Leu	Gly	755	760	765	
Thr	Ile	Lys	Met	Lys	Ala	Ile	Leu	Gly	Asp	Val	Lys	Tyr	Lys	Thr	Phe	770	775	780	
Ala	Asp	Ser	Val	Asp	Ile	Thr	Ala	Glu	Gly	Ser	Cys	Thr	Gly	Cys	Ile	785	790	795	800
Asn	Cys	Phe	Glu	Asn	Ile	His	Cys	Glu	Leu	Thr	Leu	His	Thr	Thr	Ile	805	810	815	
Glu	Ala	Ser	Cys	Pro	Ile	Lys	Ser	Ser	Cys	Thr	Val	Phe	His	Asp	Arg	820	825	830	
Ile	Leu	Val	Thr	Pro	Asn	Glu	His	Lys	Tyr	Ala	Leu	Lys	Met	Val	Cys	835	840	845	
Thr	Glu	Lys	Pro	Gly	Asn	Thr	Leu	Thr	Ile	Lys	Val	Cys	Asn	Thr	Lys	850	855	860	
Val	Glu	Ala	Ser	Met	Ala	Leu	Val	Asp	Ala	Lys	Pro	Ile	Ile	Glu	Leu	865	870	875	880
Ala	Pro	Val	Asp	Gln	Thr	Ala	Tyr	Ile	Arg	Glu	Lys	Asp	Glu	Arg	Cys	885	890	895	
Lys	Thr	Trp	Met	Cys	Arg	Val	Arg	Asp	Glu	Gly	Leu	Gln	Val	Ile	Leu				

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          900              905              910
Glu Pro Phe Lys Asn Leu Phe Gly Ser Tyr Ile Gly Ile Phe Tyr Thr
      915              920              925
Phe Ile Ile Ser Ile Val Val Leu Leu Val Ile Ile Tyr Val Leu Leu
      930              935              940
Pro Ile Cys Phe Lys Leu Arg Asp Thr Leu Arg Lys His Glu Asp Ala
945              950              955              960
Tyr Lys Arg Glu Met Lys Ile Arg
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<210> 19
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<212> PRT
<213> La Crosse virus

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Ile Trp Thr Ser Val Leu Lys Met Gln Asn Tyr Ser Thr Leu Leu Gln
      20              25              30
Leu Gly Ser Ser Ser Ser Met Pro Gln Arg Pro Arg Leu Leu Ser Arg
      35              40              45
Val Ser Gln Arg Gly Arg Leu Thr Leu Asn Leu Glu Ser Gly Arg Trp
      50              55              60
Arg Leu Ser Ile Ile Ile Phe Leu Glu Thr Gly Thr Thr Gln Leu Val
65              70              75              80
Thr Thr Ile Leu Pro Ser Thr Asp Tyr Leu Gly Ile
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<210> 20
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<213> Artificial Sequence

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<220>
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<210> 21
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<212> DNA

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<213> Artificial Sequence

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<210> 22

<211> 20

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<400> 22

tgtggtgccc gctatgatac

20

<210> 23

<211> 21

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ctgtggtgcc cgctatgata c

21

<210> 24

<211> 20

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<220>

<223> Forward primer derived from M segment of the LACV genome

<400> 24

ctgtggtgcc cgctatgata

20

<210> 25

<211> 21

<212> DNA

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<400> 25

tctgtggtgc ccgctatgat a

21

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 <400> 27
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 <210> 28
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 <400> 28
 agacagtggc actgtgacca taa 23

 <210> 29
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 <400> 29
 agacagtggc actgtgacca taat 24

 <210> 30
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<400> 33
gaagacagtg gcactgtgac cata                                     24

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<400> 34
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25

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24

<210> 37
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24

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<210> 39
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<223> Probe derived from M segment of the LACV genome

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<210> 41
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<400> 41
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<210> 42
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<400> 42
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<210> 43
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<400> 43
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<400> 52

taaccgcaga agggtcatgc accg 24

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 <210> 59
 <211> 25
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 <400> 59
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 <400> 61
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 <212> DNA
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<210> 63

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22

<210> 64

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23

<210> 65

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21

<210> 66

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24

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<210> 69
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<400> 70
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<210> 74
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<210> 75
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<400> 75
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<400> 76

tcagcacgag ttgatcagaa ca

22

<210> 77

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<400> 77

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21

<210> 78

<211> 22

<212> DNA

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<400> 78

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22

<210> 79

<211> 24

<212> DNA

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<400> 79

caagagtgtg atgtcggatt tggt

24

<210> 80

<211> 23

<212> DNA

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<223> Forward primer derived from the S segment of the LACV genome

<400> 80

aagagtgtga tgtcggattt ggt

23

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 <212> DNA
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 <400> 81
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 <210> 82
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 <400> 82
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 <210> 83
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 <400> 84
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 <210> 85
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